

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/468,011DATE: 11/14/95  
TIME: 16:05:12

INPUT SET: S7225.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Soppet, Daniel R  
Yi, Li  
Rosen, Craig A  
Ruben, Steven

ENTERED

(ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
HLTDG74

(iii) NUMBER OF SEQUENCES: 8

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
Stewart & Olstein  
(B) STREET: 6 Becker Farm Road  
(C) CITY: Roseland  
(D) STATE: NJ  
(E) COUNTRY: USA  
(F) ZIP: 07068-1739

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/468,011  
(B) FILING DATE: 06-JUN-1995  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ferraro, Gregory D  
(B) REGISTRATION NUMBER: 36,134  
(C) REFERENCE/DOCKET NUMBER: 325800-458

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700  
(B) TELEFAX: 201-994-1744

## (2) INFORMATION FOR SEQ ID NO:1:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/468,011

DATE: 11/14/95  
TIME: 16:05:16

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 2003 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: single
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55
56      (ix) FEATURE:
57          (A) NAME/KEY: CDS
58          (B) LOCATION: 90..1712
59
60
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63      GTTTGCTCTG GGCAGCCAAG TTGGCATATT GGAAGCTTTT TCCGGGCTCT GGAGGAGGGT      60
64
65      CCCTGCTTCT TCCTACAGCC GTTCCGGGC ATG GCC TGG CTG GGG GCG TCG CTC      113
66          Met Ala Trp Leu Gly Ala Ser Leu
67          1 5
68
69      CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC      161
70      His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
71          10 15 20
72
73      CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT      209
74      Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
75          25 30 35 40
76
77      GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC      257
78      Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
79          45 50 55
80
81      CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT      305
82      Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
83          60 65 70
84
85      TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT      353
86      Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
87          75 80 85
88
89      TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC      401
90      Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
91          90 95 100
92
93      CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC      449
94      Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
95          105 110 115 120
96
97      AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA      497
98      Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
99          125 130 135

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100																	
101	AAG	CAA	GAA	TTC	TGT	GAA	CGC	CTC	TAT	GTA	ATG	TAT	ACC	GTT	GGC	TAC	545
102	Lys	Gln	Glu	Phe	Cys	Glu	Arg	Leu	Tyr	Val	Met	Tyr	Thr	Val	Gly	Tyr	
103				140					145					150			
104																	
105	TCC	ATC	TCT	TTT	GGT	TCC	TTG	GCT	GTG	GCT	ATT	CTC	ATC	ATT	GGT	TAC	593
106	Ser	Ile	Ser	Phe	Gly	Ser	Leu	Ala	Val	Ala	Ile	Leu	Ile	Ile	Gly	Tyr	
107			155					160					165				
108																	
109	TTC	AGA	CGA	TTG	CAT	TGC	ACT	AGG	AAC	TAT	ATC	CAC	ATG	CAC	TTA	TTT	641
110	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	
111		170					175					180					
112																	
113	GTG	TCT	TTC	ATG	CTG	AGA	GCT	ACA	AGC	ATC	TTT	GTC	AAA	GAC	AGA	GTA	689
114	Val	Ser	Phe	Met	Leu	Arg	Ala	Thr	Ser	Ile	Phe	Val	Lys	Asp	Arg	Val	
115	185					190					195					200	
116																	
117	GTC	CAT	GCT	CAC	ATA	GGA	GTA	AAG	GAG	CTG	GAG	TCC	CTA	ATA	ATG	CAG	737
118	Val	His	Ala	His	Ile	Gly	Val	Lys	Glu	Leu	Glu	Ser	Leu	Ile	Met	Gln	
119					205					210					215		
120																	
121	GAT	GAC	CCA	CAA	AAT	TCC	ATT	GAG	GCA	ACT	TCT	GTG	GAC	AAA	TCA	CAA	785
122	Asp	Asp	Pro	Gln	Asn	Ser	Ile	Glu	Ala	Thr	Ser	Val	Asp	Lys	Ser	Gln	
123				220					225					230			
124																	
125	TAT	ATC	GGG	TGC	AAG	ATT	GCT	GTT	GTG	ATG	TTT	ATT	TAC	TTC	CTG	GCT	833
126	Tyr	Ile	Gly	Cys	Lys	Ile	Ala	Val	Val	Met	Phe	Ile	Tyr	Phe	Leu	Ala	
127			235					240					245				
128																	
129	ACA	AAT	TAT	TAT	TGG	ATC	CTG	GTG	GAA	GGT	CTC	TAC	CTG	CAT	AAT	CTC	881
130	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu	
131		250					255					260					
132																	
133	ATC	TTT	GTG	GCT	TTC	TTT	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929
134	Ile	Phe	Val	Ala	Phe	Phe	Ser	Asp	Thr	Lys	Tyr	Leu	Trp	Gly	Phe	Ile	
135	265					270					275					280	
136																	
137	TTG	ATA	GGC	TGG	GGG	TTT	CCA	GCA	GCA	TTT	GTT	GCA	GCA	TGG	GCT	GTG	977
138	Leu	Ile	Gly	Trp	Gly	Phe	Pro	Ala	Ala	Phe	Val	Ala	Ala	Trp	Ala	Val	
139					285					290					295		

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153	TGG GAG ACC AAT GCA GTT GGG CAT GAC ACA AGG AAG CAA TAC AGG AAA	1169
154	Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys	
155	345 350 355 360	
156		
157	CTG GCC AAA TCG ACA CTG GTC CTG GTC CTA GTC TTT GGA GTG CAT TAC	1217
158	Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr	
159	365 370 375	
160		
161	ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG	1265
162	Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu	
163	380 385 390	
164		
165	ATC CGC ATG CAC TGT GAG CTC TTC TTC AAC TCC TTT CAG GGT TTC TTT	1313
166	Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe	
167	395 400 405	
168		
169	GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG	1361
170	Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val	
171	410 415 420	
172		
173	AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA	1409
174	Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr	
175	425 430 435 440	
176		
177	CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG	1457
178	Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr	
179	445 450 455	
180		
181	CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC	1505
182	His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys	
183	460 465 470	
184		
185	TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC	1553
186	Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala	
187	475 480 485	
188		
189	ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC	1601
190	Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala	
191	490 495 500	
192		
193	TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG	1649
194	Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln	
195	505 510 515 520	
196		
197	AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC	1697
198	Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn	
199	525 530 535	
200		
201	CCA GAC ACT GAA GGA TGACAAGGAG AACTGAGGA TGTTCTCTGA ATGGACATGT	1752
202	Pro Asp Thr Glu Gly	
203	540	
204		
205	GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT	1812

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/468,011

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206  
207 CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTAATAATA ATAGTTTTTA 1872  
208  
209 GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT 1932  
210  
211 AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT 1992  
212  
213 GTGATTGTTC A 2003  
214  
215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

226  
227 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu  
228 1 5 10 15  
229  
230 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile  
231 20 25 30  
232  
233 Thr Ile Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys  
234 35 40 45  
235  
236 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe  
237 50 55 60  
238  
239 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys  
240 65 70 75 80  
241  
242 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys  
243 85 90 95  
244  
245 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met  
246 100 105 110  
247  
248 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe  
249 115 120 125  
250  
251 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu  
252 130 135 140  
253  
254 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala  
255 145 150 155 160  
256  
257 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg  
258 165 170 175

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/468,011**

DATE: 11/14/95  
TIME: 16:05:30

*INPUT SET: S7225.raw*

Line

Error

Original Text